

SEQUENCE LISTING

<110> Bandaru, Rajasekhar

<120> 68730 and 69112, Protein Kinase
Molecules and Uses Therefor

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Pro Arg Arg Ala Pro Gly Ala Pro Ser Pro Ala Arg Pro Arg Pro Leu
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ctc cgc gcc gcg ctc gtc ggc cat ggc ccg gga gaa ccg cga gag cag 194
Leu Arg Ala Ala Leu Val Gly His Gly Pro Gly Glu Arg Arg Glu Gln
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Leu Leu Leu Glu Lys Ala Ser * Arg His Gln Glu Asp Leu Arg Val
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Gly Ala Glu Gly Gln Gly Lys Gln His Arg Glu * Asp Ser Arg Pro	
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Glu Lys Asp * Ala * Lys Tyr Cys Cys Pro Gly Arg His Leu *	
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Pro Glu Lys Leu Cys Gln Glu Gln Met Glu Thr Ser Ile * Cys His	
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Gly Arg Arg Glu Thr Tyr Glu Lys Thr Thr Pro Arg Gln Gln Pro Gly	
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 65 70 75 80
 Pro Arg Asn Arg Gly Leu Phe Arg Ser Gly Phe Ser Arg Glu Gly Asn
 85 90 95
 Trp Gln Ala Leu Cys Cys Glu Val Tyr Pro Glu Gly Ala Glu Gly Gln
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 Gly Lys Gln His Arg Glu Asp Ser Arg Pro Glu Lys Asp Ala Lys Tyr
 115 120 125
 Cys Cys Pro Gly Arg His Leu Lys Pro Lys Ser Pro Val Leu Gly His

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Gln	Gln	Ser	Arg	Leu	Leu	Val	His	Arg	Ser	Asp	Cys	Leu	His	Leu	Ala
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Ala Val Glu Glu Leu Tyr Pro Asn Lys Ala Arg Ala Leu Thr Leu Ala
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cag cac agc cgt gcc cct tct cca agg ctg agg agc agg ctg ttt agc 1347
Gln His Ser Arg Ala Pro Ser Pro Arg Leu Arg Ser Arg Leu Phe Ser
30 35 40 45

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Lys Ala Leu Lys Gly Asp His Arg Cys Gly Glu Thr Glu Thr Pro Lys
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	Arg Glu Ala Thr Leu Glu Glu Arg His Ala Arg Gly Glu Lys His Leu			
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	Gly Val Glu Ile Glu Lys Thr Ser Gly Glu Ile Ile Arg Cys Glu Lys			
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	Ser Leu Gly Thr Ser Glu Leu Asp Met Gly Lys Gly Pro Met Tyr Asp			
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	gag gag ggg ctg agg gag gtg aag aag gac acc agg ccc atg agc agg			2019
	Glu Glu Gly Leu Arg Glu Val Lys Lys Asp Thr Arg Pro Met Ser Arg			
	255	260	265	
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<210> 7

<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus sequence involved in ATP binding

<221> VARIANT
<222> 1
<223> The L at position 1 can be I or V.

<221> VARIANT
<222> 3
<223> The amino acid at position 3 can be any amino acid
except P

<221> VARIANT
<222> 5
<223> The amino acid at position 3 can be any amino acid
except P

<221> VARIANT
<222> 6
<223> The F at position 6 can be Y, W, M,G, S, T, N, or
H

<221> VARIANT
<222> 7
<223> The S at position 7 can be G or A

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 can be any amino acid
except P or W.

<221> VARIANT
<222> (9)...(0)
<223> The L at position 9 can be I, V, C, A, or T.

<221> VARIANT
<222> (10)...(0)
<223> The amino acid at position 10 can be any amino
acid except P or D.

<221> VARIANT
<222> (11)...(0)
<223> The amino acid at position 11 can be any amino
acid.

<221> VARIANT
<222> (12)...(0)

<223> The G at position 12 can be S, T, A, C, L, I, V, M, F, or Y.

<221> VARIANT

<222> (13)...(0)

<223> The amino acid at position 13 is as few as 5, up to 18, amino acids, and the amino acid can be any amino acid.

<221> VARIANT

<222> (14)...(0)

<223> The L at position 14 can be I, V, M, F, Y, W, C, S, T, A, or R.

<221> VARIANT

<222> (15)...(0)

<223> The A at position 15 can be I, V, or P.

<221> VARIANT

<222> (16)...(0)

<223> The L at position 16 can be I, V, I, M, F, A, G, C, K, or R.

<400> 7

Leu Gly Xaa Gly Xaa Phe Ser Xaa Leu Xaa Xaa Gly Xaa Leu Ala Leu
1 5 10 15
Lys

<210> 8

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence for Serine/Threonine Kinase

<221> VARIANT

<222> 1

<223> The L at position 1 can be I, V, M, F, or Y.

<221> VARIANT

<222> 2

<223> The amino acid at position 2 can be any amino acid.

<221> VARIANT

<222> 3

<223> The H at position 3 can be Y.

<221> VARIANT

<222> 4

<223> The amino acid at position 4 can be any amino acid.

<221> VARIANT

<222> 5

<223> The D at position 5 is an active site residue.

<221> VARIANT

<222> (6)...(0)

<223> The L at position 6 can be I, V, M, F, Y.

<221> VARIANT

<222> (8)...(0)

<223> The amino acid at position 8 is two amino acids, and can be any amino acid.

<221> VARIANT

<222> (10)...(0)

<223> The L at position 10 can be any 3 of L, I, V, M, F, Y, C, T.

<400> 8

Leu Xaa His Xaa Asp Leu Lys Xaa Asn Leu
1 5 10

<210> 9

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus Sequence for Tyrosine Kinase

<221> VARIANT

<222> 1

<223> The L at position 1 can be I, V, M, F, Y, or C.

<221> VARIANT

<222> 2

<223> The amino acid at position 2 can be any amino acid.

<221> VARIANT

<222> 3

<223> The H at position 3 can be Y.

<221> VARIANT

<222> 4

<223> The amino acid at position 4 can be any amino acid.

<221> VARIANT

<222> 5

<223> The D at position 5 is an active site residue.

<221> VARIANT
<222> (6)...(0)
<223> The L at position 6 can be I, V, M, F, or Y.

<221> VARIANT
<222> (7)...(0)
<223> The R at position 7 can be S, T, A, or C.

<221> VARIANT
<222> (8)...(0)
<223> The amino acid at position 8 is 2 amino acids, and
can be any amino acid.

<221> VARIANT
<222> (10)...(0)
<223> The L at position 10 can be any 3 of L, I, V, M,
F, Y, or C.

<400> 9
Leu Xaa His Xaa Asp Leu Arg Xaa Asn Leu
1 5 10

<210> 10
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Consensus Sequence for Tyrosine Kinase
Phosphorylation Site

<221> VARIANT
<222> 1
<223> The R at position 1 can be K.

<221> VARIANT
<222> 2
<223> The amino acid at position 2 can be two or three
amino acids, and the amino acid can be any amino
acid.

<221> VARIANT
<222> (3)...(0)
<223> The D at position 3 can be E.

<221> VARIANT
<222> 4
<223> The amino acid at position 2 can be two or three
amino acids, and the amino acid can be any amino
acid.